# SEQUENCE LISTING

<110> Japan Science and Technology Corporation

<120> Method for Producing an Antibody with Genetic Immunization

<130> 01F033PCT

<140> PCT/JP01/06371
<141> 2001-07-24

<150> JP2000-222743
<151> 2000-07-24

<150> JP2000-254407
<151> 2000-08-24

<160> 13

<170> PatentIn Ver. 2.1

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<222> (151).. (600)

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aatcaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt 174
Met Met Thr Lys His Lys Lys Cys
1 5

ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata 222
Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
10 15 20

gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270
Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile

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 25                  30                  35                  40

ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg   318
Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
                45                  50                  55

aat tca agt aaa tac aac tgt tcc act caa cat gcc gac cta act ata   366
Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
            60                  65                  70

att gac aac ata gaa gaa atg aat ttt ctt agg cgg tat aaa tgc agt   414
Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
        75                  80                  85

tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa   462
Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln
    90                  95                  100

tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt   510
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser
105                 110                 115                 120

gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt   558
Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys
                125                 130                 135

tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa           600
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His
            140                 145                 150

gttaatgtct aagataatgg ggaaaataga aaataacatt attaagtgta aaaccagcaa 660

agtacttttt taattaaaca aagttcgagt tttgtac                          697


<210> 2
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<212> PRT
<213> Homo sapiens

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Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
            20                  25                  30
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Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
         35                  40                  45
Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
     50                  55                  60
Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
 65                  70                  75                  80
Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
                 85                  90                  95
Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
            100                 105                 110
Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
        115                 120                 125
Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
    130                 135                 140
Arg Lys Arg Ile His
145
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<210> 3
<211> 548
<212> DNA
<213> Homo sapiens

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<222> (30).. (503)

<400> 3

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                               Met Ala Thr Pro Pro Lys Arg Arg
                                 1               5

gcg gtg gag gcc acg ggg gag aaa gtg ctg cgc tac gag acc ttc atc   101
Ala Val Glu Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile
     10                  15                  20

agt gac gtg ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac   149
Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp
 25                  30                  35                  40

aag gta tat gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att   197
Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile
                 45                  50                  55
```

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gag cga ctc cag gaa gct aag cac tcg gag tta tat atg cag gtg gat   245
Glu Arg Leu Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp
            60                  65                  70

ttg ggc tgt aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc   293
Leu Gly Cys Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg
        75                  80                  85

atc tat gtg gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca   341
Ile Tyr Val Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala
    90                  95                  100

gaa gct ctc aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc   389
Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu
105                 110                 115                 120

agc aac agc ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac   437
Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His
                125                 130                 135

atg ttg cta gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca   485
Met Leu Leu Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro
            140                 145                 150

gag aag cct cac cat tga cttcttcccc ccatcctcag acattaaaga          533
Glu Lys Pro His His
        155

gcctgaatgc ctttg                                                  548
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Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
            20                  25                  30
Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
        35                  40                  45
Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
    50                  55                  60
```

```
Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
 65                  70                  75                  80
Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
                 85                  90                  95
Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
            100                 105                 110
Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
        115                 120                 125
Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
    130                 135                 140
Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
145                 150                 155
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<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence: Synthesized oligonucleotide

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cccgatatct catggcgacg ccccctaagc 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence: Synthesized oligonucleotide

<400> 6
cccgatatct caatggtgag gcttctctgg 30

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence: Synthesized oligonucleotide

<400> 7
cccgaattca tggcgacgcc ccctaagc 28

<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence: Synthesized oligonucleotide

<400> 8
cccgtcgacg catggtgagg cttctctggg aa 32

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<222> (25).. (915)

<400> 9
aacatctggg gacagcggga aaac atg agt gac tcc aag gaa cca agg gtg 51
Met Ser Asp Ser Lys Glu Pro Arg Val
1 5

cag cag ctg ggc ctc ctg ggg tgt ctt ggc cat ggc gcc ctg gtg ctg 99
Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu
10 15 20 25

caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt 147
Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu
30 35 40

gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag 195
Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu
45 50 55

caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt 243
Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly
60 65 70

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gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc   291
Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
     75                  80                  85

cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag   339
Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
 90                  95                 100                 105

gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg   387
Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
                110                 115                 120

cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg   435
Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
            125                 130                 135

aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc   483
Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile
        140                 145                 150

tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag   531
Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
    155                 160                 165

aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct   579
Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala
170                 175                 180                 185

gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag   627
Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln
                190                 195                 200

gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc   675
Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser
            205                 210                 215

aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt   723
Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe
        220                 225                 230

gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga   771
Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly
    235                 240                 245
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aac tgt tac ttc atg tct aac tcc cag cgg aac tgg cac gac tcc gtc   819
Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val
250                 255                 260                 265

acc gcc tgc cag gaa gtg agg gcc cag ctc gtc gta atc aaa act gct   867
Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala
                270                 275                 280

gag gag cag ctt cca gcg gta ctg gaa cag tgg aga acc caa caa tag   915
Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln
            285                 290                 295

cgggaatgaa gactgtgcgg aatttagtgg cagtggctgg aacgacaatc gatgtgacgt 975

tgacaattac tggatctgca aaaagcccgc agcctgcttc agagacgaat agttgtttcc 1035

ctgctagcct cagcctccat tgtggtatag cagaacttca cccacttgta agccagcgct 1095

tcttctctcc atccttggac cttcacaaat gccctgagac ggttctctgt tcgatttttc 1155

atcccctatg aacctgggtc ttattctgtc cttctgatgc ctccaagttt ccctggtgta 1215

gagcttgtgt tcttggccca tccttggagc tttataagtg acctgagtgg gatgcattta 1275

gggggcgggc ttggtatgtt gtatgaatcc actctctgtt ccttttggag attagactat 1335

ttggattcat gtgtagctgc cctgtcccct ggggctttat ctcatccatg caaactacca 1395

tctgctcaac ttccagctac accccgtgca ccctttttgac tggggacttg ctggttgaag 1455

gagctcatct tgcaggctgg aagcaccagg gaattaattc ccccagtcaa ccaatggcat 1515

ccagagaggg catggaggct ccatacaacc tcttccaccc ccacatcttt ctttgtccta 1575

tacatgtctt ccatttggct gtttctgagt tgtagccttt ataataaagt ggtaaatgtt 1635

gtaactgc                                                          1643
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<222> (118).. (1236)

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atg aag tat ctc cgg cac cgg cgg ccc aat gcc acc ctc att ctg gcc 165
Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
1 5 10 15

atc ggc gct ttc acc ctc ctc ctc ttc agt ctg cta gtg tca cca ccc 213
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
20 25 30

acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc 261
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
35 40 45

tgg ccc act cca ccc acc cgc cca gcc ccg gcc ccg tgc cat gcc aac 309
Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
50 55 60

acc tct atg gtc acc cac ccg gac ttc gcc acg cag ccg cag cac gtt 357
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
65 70 75 80

cag aac ttc ctc ctg tac aga cac tgc cgc cac ttt ccc ctg ctg cag 405
Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
85 90 95

gac gtg ccc ccc tct aag tgc gcg cag ccg gtc ttc ctg ctg ctg gtg 453
Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val
100 105 110

atc aag tcc tcc cct agc aac tat gtg cgc cgc gag ctg ctg cgg cgc 501
Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg
115 120 125

acg tgg ggc cgc gag cgc aag gta cgg ggt ttg cag ctg cgc ctc ctc 549
Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu
130 135 140

ttc ctg gtg ggc aca gcc tcc aac ccg cac gag gcc cgc aag gtc aac 597

```
Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn
145                 150                 155                 160

cgg ctg ctg gag ctg gag gca cag act cac gga gac atc ctg cag tgg   645
Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp
                165                 170                 175

gac ttc cac gac tcc ttc ttc aac ctc acg ctc aag cag gtc ctg ttc   693
Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe
            180                 185                 190

tta cag tgg cag gag aca agg tgc gcc aac gcc agc ttc gtg ctc aac   741
Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn
        195                 200                 205

ggg gat gat gac gtc ttt gca cac aca gac aac atg gtc ttc tac ctg   789
Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu
    210                 215                 220

cag gac cat gac cct ggc cgc cac ctc ttc gtg ggg caa ctg atc caa   837
Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln
225                 230                 235                 240

aac gtg ggc ccc atc cgg gct ttt tgg agc aag tac tat gtg cca gag   885
Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu
                245                 250                 255

gtg gtg act cag aat gag cgg tac cca ccc tat tgt ggg ggt ggt ggc   933
Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly
            260                 265                 270

ttc ttg ctg tcc cgc ttc acg gcc gct gcc ctg cgc cgt gct gcc cat   981
Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His
        275                 280                 285

gtc ttg gac atc ttc ccc att gat gat gtc ttc ctg ggt atg tgt ctg   1029
Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu
    290                 295                 300

gag ctt gag gga ctg aag cct gcc tcc cac agc ggc atc cgc acg tct   1077
Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser
305                 310                 315                 320

ggc gtg cgg gct cca tcg caa cac ctg tcc tcc ttt gac ccc tgc ttc   1125
Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe
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                325                 330                 335

tac cga gac ctg ctg ctg gtg cac cgc ttc cta cct tat gag atg ctg   1173
Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu
            340                 345                 350

ctc atg tgg gat gcg ctg aac cag ccc aac ctc acc tgc ggc aat cag   1221
Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln
        355                 360                 365

aca cag atc tac tga gtcagcatca gggtccccag cctctgggct cctgtttcca   1276
Thr Gln Ile Tyr
    370

taggaagggg cgacaccttc ctcccaggaa gctgagacct ttgtggtctg agcataaggg 1336

agtgccaggg aaggtttgag gtttgatgag tgaatattct ggctggcgaa ctcctacaca 1396

tccttcaaaa cccacctggt actgttccag catcttccct ggatggctgg aggaactcca 1456

gaaaatatcc atcttctttt tgtggctgct aatggcagaa gtgcctgtgc tagagttcca 1516

actgtggatg catccgtccc gtttgagtca aagtcttact tccctgctct cacctactca 1576

cagacgggat gctaagcagt gcacctgcag tggtttaatg gcagataagc tccgtctgca 1636

gttccaggcc agccagaaac tcctgtgtcc acatagagct gacgtgagaa atatctttca 1696

gcccaggaga gaggggtcct gatcttaacc ctttcctggg tctcagacaa ctcagaaggt 1756

tgggggggata ccagagaggt ggtggaatag gaccgccccc tccttacttg tgggatcaaa 1816

tgctgtaatg gtggaggtgt gggcagagga gggaggcaag tgtcctttga aagttgtgag 1876

agctcagagt ttctggggtc ctcattagga gcccccatcc ctgtgttccc caagaattca 1936

gagaacagca ctggggctgg aatgatcttt aatgggccca aggccaacag gcatatgcct 1996

cactactgcc tggagaaggg agagattcag gtcctccagc agcctccctc acccagtatg 2056

ttttacagat tacgggggga ccgggtgagc cagtgacccc ctgcagcccc cagcttcagg 2116

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aaattttgtg                                                       2186
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<213> Homo sapiens

<220>
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<222> (145).. (693)

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aagtgagagt ccagcggtct tccagcgctt gggccacggc ggcggccctg ggagcagagg 120

tggagcgacc ccattacgct aaag atg aaa ggc tgg ggt tgg ctg gcc ctg 171
Met Lys Gly Trp Gly Trp Leu Ala Leu
1 5

ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 219
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
10 15 20 25

ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa 267
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
30 35 40

att gcc cag gtg gac ccc aag aag acc att cag atg gga tct ttc cgg 315
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
45 50 55

atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat gcc cgc 363
Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr Ala Arg
60 65 70

tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac cgg atg 411
Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp Arg Met
75 80 85

aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag aac tac 459
Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys Asn Tyr
90 95 100 105

gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac cta caa 507

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Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp Leu Gln
                110                 115                 120

ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt gcg tgt   555
Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe Ala Cys
            125                 130                 135

gag agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc ttt tcc   603
Glu Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe Phe Ser
        140                 145                 150

cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga aca gat   651
Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg Thr Asp
    155                 160                 165

ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta tga           693
Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu
170                 175                 180

accactggag cagcccacac tggcttgatg gatcaccccc aggaggggaa aatggtggca 753

atgcctttta tatattatgt ttttactgaa attaactgaa aaaatatgaa accaaaagta 813

c                                                                  814
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<212> DNA
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<222> (73).. (564)

<400> 12

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tgacacggaa gc atg cga cgg ctg ctg atc cct ctg gcc ctg tgg ctg ggc 111
             Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
               1               5                  10

gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc   159
Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
     15                  20                  25
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ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg   207
Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
 30                  35                  40                  45

gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca   255
Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
                50                  55                  60

gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc   303
Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
            65                  70                  75

cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg   351
Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
        80                  85                  90

agg aaa cgg aaa tgc ctg gcc tgc atc aaa ctg ggc tct gag gac aaa   399
Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
    95                  100                 105

gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg   447
Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg
110                 115                 120                 125

gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct   495
Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala
                130                 135                 140

ggt gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc   543
Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser
            145                 150                 155

aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg      594
Lys Ala Leu Pro Arg Ser
        160

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ccccagccat gataataaag ctgctctccc agctgcctct c                     695
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Met Arg Leu Thr
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cgg aag cgg ctc tgc tcg ttt ctt atc gcc ctg tac tgc cta ttc tcc 164
Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr Cys Leu Phe Ser
5 10 15 20

ctc tac gct gcc tac cac gtc ttc ttc ggg cgc cgc cgc cag gcg ccg 212
Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg Arg Gln Ala Pro
25 30 35

gcc ggg tcc ccg cgg ggc ctc agg aag ggg gcg gcc ccc gcg cgg gag 260
Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala Pro Ala Arg Glu
40 45 50

aga cgc ggc cga gaa cag tcc act ttg gaa agt gaa gaa tgg aat cct 308
Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu Glu Trp Asn Pro
55 60 65

tgg gaa gga gat gaa aaa aat gag caa caa cac aga ttt aaa act agc 356
Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser
70 75 80

ctt caa ata tta gat aaa tcc acg aaa gga aaa aca gat ctc agt gta 404
Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val
85 90 95 100

caa atc tgg ggc aaa gct gcc att ggc ttg tat ctc tgg gag cat att 452
Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu Trp Glu His Ile
105 110 115

ttt gaa ggc tta ctt gat ccc agc gat gtg act gct caa tgg aga gaa 500
Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala Gln Trp Arg Glu
120 125 130

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gga aag tca atc gta gga aga aca cag tac agc ttc atc act ggt cca   548
Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe Ile Thr Gly Pro
        135                 140                 145

gct gta ata cca ggg tac ttc tcc gtt gat gtg aat aat gtg gta ctc   596
Ala Val Ile Pro Gly Tyr Phe Ser Val Asp Val Asn Asn Val Val Leu
    150                 155                 160

att tta aat gga aga gaa aaa gca aag atc ttt tat gcc acc cag tgg   644
Ile Leu Asn Gly Arg Glu Lys Ala Lys Ile Phe Tyr Ala Thr Gln Trp
165                 170                 175                 180

tta ctt tat gca caa aat tta gtg caa att caa aaa ctc cag cat ctt   692
Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys Leu Gln His Leu
                185                 190                 195

gct gtt gtt ttg ctc gga aat gaa cat tgt gat aat gag tgg ata aac   740
Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn Glu Trp Ile Asn
            200                 205                 210

cca ttc ctc aaa aga aat gga ggc ttc gtg gag ctg ctt ttc ata ata   788
Pro Phe Leu Lys Arg Asn Gly Gly Phe Val Glu Leu Leu Phe Ile Ile
        215                 220                 225

tat gac agc ccc tgg att aat gac gtg gat gtt ttt cag tgg cct tta   836
Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe Gln Trp Pro Leu
    230                 235                 240

gga gta gca aca tac agg aat ttt cct gtg gtg gag gca agt tgg tca   884
Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser
245                 250                 255                 260

atg ctg cat gat gag agg cca tat tta tgt aat ttc tta gga acg att   932
Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile
                265                 270                 275

tat gaa aat tca tcc aga cag gca cta atg aac att ttg aaa aaa gat   980
Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp
            280                 285                 290

ggg aac gat aag ctt tgt tgg gtt tca gca aga gaa cac tgg cag cct   1028
Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu His Trp Gln Pro
        295                 300                 305

cag gaa aca aat gaa agt ctt aag aat tac caa gat gcc ttg ctt cag   1076
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Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln
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agt gat ctc aca ttg tgc ccg gtc gga gta aac aca gaa tgc tat cga   1124
Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg
325                 330                 335                 340

atc tat gag gct tgc tcc tat ggc tcc att cct gtg gtg gaa gac gtg   1172
Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val Val Glu Asp Val
                345                 350                 355

atg aca gct ggc aac tgt ggg aat aca tct gtg cac cac ggt gct cct   1220
Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His His Gly Ala Pro
            360                 365                 370

ctg cag tta ctc aag tcc atg ggt gct ccc ttt atc ttt atc aag aac   1268
Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn
        375                 380                 385

tgg aag gaa ctc cct gct gtt tta gaa aaa gag aaa act ata att tta   1316
Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu
    390                 395                 400

caa gaa aaa att gaa aga aga aaa atg tta ctt cag tgg tat cag cac   1364
Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His
405                 410                 415                 420

ttc aag aca gag ctt aaa atg aaa ttt act aat att tta gaa agc tca   1412
Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser
                425                 430                 435

ttt tta atg aat aat aaa agt taa ttatcttttt gagct                 1451
Phe Leu Met Asn Asn Lys Ser
            440
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